GenCore version 5.1.3

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 14, 2003, 00:32:25 ; Search time 388.449 Seconds
(without alignments)
1495.730 Million cell updates/sec

Title: US-09-698-781-3
Perfect score: 1436
Sequence: 1 MKQILHPALETTAMTLFPVL.....KHQLVRDSCKASCNCSNSIY 258

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09698781_@CGN_1_1_338_@runat_07032003_083458_5317 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1436	100.0	2144	22	AAD06222	Human full-length
	2	1433	99.8	1610	23	ABV24823	Human prostate exp
	3	1428	99.4	2133	22	AAH98651	Human EST-derived
	4	1428	99.4	2133	22	AAH98659	Human EST-derived
	5	1428	99.4	2452	23	ABV22644	Human prostate exp
	6	1428	99.4	2452	23	ABV24631	Human prostate exp
	7	1428	99.4	2452	23	ABV25272	Human prostate exp
	8	1428	99.4	2452	23	ABV25706	Human prostate exp
	9	1428	99.4	2452	23	ABV28467	Human prostate exp
	10	1428	99.4	2452	23	ABV28648	Human prostate exp
	11	1386	96.5	2128	24	ABL67806	Oesophagus cancer
	12	1002	69.8	1386	23	AAS70843	DNA encoding novel
	13	1002	69.8	1386	23	AAS92411	DNA encoding novel
c	14	683	47.6	534	23	ABV43214	Human prostate exp
	15	535.5	37.3	683	23	AAS70842	DNA encoding novel
	16	535.5	37.3	683	23	AAS92408	DNA encoding novel
	17	500	34.8	372	23	ABV13234	Human prostate exp
	18	494	34.4	395	23	ABV34353	Human prostate exp
	19	400.5	27.9	395	23	ABV38239	Human prostate exp
c	20	400	27.9	540	23	ABV08906	Human prostate exp
	21	399	27.8	343	23	ABV08331	Human prostate exp
c	22	397	27.6	430	23	ABV08865	Human prostate exp
c	23	397	27.6	451	23	ABV38756	Human prostate exp
	24	396	27.6	400	23	ABV07202	Human prostate exp
	25	396	27.6	633	23	ABV37142	Human prostate exp
c	26	356.5	24.8	530	23	ABV38795	Human prostate exp
	27	354	24.7	263	20	AAX40711	Human secreted pro
	28	337.5	23.5	1008	24	AAD30356	Mouse testes-speci
	29	318	22.1	3804	21	AAC77617	Human cancer assoc
	30	305.5	21.3	882	22	AAS21374	Human cDNA sequenc
	31	304.5	21.2	880	21	AAI72857	cDNA clone APPLE,
	32	300.5	20.9	759	24	ABL57727	Human sbg1002620TI
	33	300	20.9	427	23	AAS70845	DNA encoding novel
	34	296.5	20.6	939	22	AAH98687	Rat EST-derived co
	35	296.5	20.6	1690	22	AAH15690	Human cDNA sequenc
	36	296.5	20.6	1824	24	ABK33563	cDNA encoding huma
	37	296.5	20.6	2272	22	AAF77687	Human protease-inh
	38	296.5	20.6	3836	24	AAL39682	Human secreted pro
c	39	296.5	20.6	4877	22	AAS60871	Human cancer agent
c	40	296.5	20.6	4877	22	AAS60872	Human cancer agent
c	41	296.5	20.6	4877	22	AAS60883	Human cancer agent
	42	296	20.6	2403	22	AAD17766	Human novel trypsi
	43	295.5	20.6	1491	22	AAF77686	Human protease-inh
	44	295.5	20.6	1494	24	ABL57728	Human sbg1002620TI
	45	295.5	20.6	1669	22	AAD17765	Human novel trypsi

ALIGNMENTS

RESULT 1
AAD06222
ID AAD06222 standard; cDNA; 2144 BP.
XX
AC AAD06222;
XX
DT 31-JUL-2001 (first entry)
XX
DE Human full-length 36P1G3/SGP28 cDNA.
XX
KW Human; 36P1G3 clone; specific granule protein 28; SGP28; therapy;
KW prostate; colon; cancer; prognosis; vaccine; anticancer; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 3..779
FT /*tag= a

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FT                   /product= "Human full-length 36P1G3/SGP28 protein"
FT   sig_peptide     3..98
FT                   /*tag=  b
FT   mat_peptide     99..776
FT                   /*tag=  c
FT                   /product= "Human mature full-length 36P1G3/SGP28 protein"
XX
PN   WO200131343-A2.
XX
PD   03-MAY-2001.
XX
PF   27-OCT-2000; 2000WO-US29607.
XX
PR   28-OCT-1999;   99US-0162610.
XX
PA   (UROG-) UROGENESYS INC.
XX
PI   Hubert RS,  Raitano AB,  Afar DEH,  Mitchell SC,  Faris M;
PI   Jakobovits A;
XX
DR   WPI; 2001-308685/32.
DR   P-PSDB; AAE02211.
XX
PT   Detecting cancers, particularly of prostate and colon, from
PT   overexpression of SGP28 protein, also methods for treating these
PT   cancers e.g. by vaccination with the protein  -
XX
PS   Claim 16; Page 62-63; 102pp; English.
XX
CC   The present invention relates to methods and compositions for the
CC   diagnosis and therapy of prostate cancer which utilise human SGP28
CC   (specific granule protein 28) gene and proteins. The method involves
CC   detecting cancers, particularly of prostate and colon, from
CC   overexpression of SGP28 protein. The expression of SGP28, which is an
CC   extracellular protein is restricted to the prostate and ovary, and is
CC   markedly up-regulated in prostate tumours. SGP28 sequence is used for
CC   diagnosis (including in vivo imaging), staging, monitoring and prognosis
CC   of prostatic and colon cancer, and for assisting selection of therapy.
CC   Also SGP28-expressing cancers can be treated by administering a
CC   composition or vaccine that contains a vector expressing an antibody
CC   specific for SGP28 protein, nucleic acid encoding SGP28 protein or its
CC   fragments, polypeptides encoded by SGP28 gene and SGP28-specific antibody
CC   optionally conjugated to toxin or therapeutic agent. SGP28 gene product
CC   is also used as source of therapeutic antisense or ribozyme agents, as
CC   primers/probes for diagnosis or prognosis, to identify compounds that
CC   inhibit calcium entry into prostatic cells, for recombinant production
CC   of SGP28 peptides and for isolating related sequences. SGP28 protein and
CC   its fragments are used to raise specific antibodies (Ab) and to identify
CC   specific binding agents (potentially useful as therapeutic and
CC   diagnostic agents) and also potential anticancer agents. The present
CC   sequence is human full-length 36P1G3/SGP28 cDNA.
XX
SQ   Sequence 2144 BP; 735 A; 403 C; 382 G; 624 T; 0 other;

Alignment Scores:
Pred. No.:              1.8e-136      Length:          2144
Score:                  1436.00       Matches:         258
Percent Similarity:     100.00%       Conservative:    0
Best Local Similarity:  100.00%       Mismatches:      0
Query Match:            100.00%       Indels:          0
DB:                     22            Gaps:            0

US-09-698-781-3 (1-258) x AAD06222 (1-2144)

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Db       3 ATGAAACAAATACTTCATCCTGCTCTGGAAACCACTGCAATGACATTATTCCCAGTGCTG 62

Qy      21 LeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAla 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      63 TTGTTCCTGGTTGCTGGGCTGCTTCCATCTTTTCCAGCAAATGAAGATAAGGATCCCGCT 122

Qy      41 PheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsn 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123 TTTACTGCTTTGTTAACCACCCAAACACAAGTGCAAAGGGAGATTGTGAATAAGCACAAT 182

Qy      61 GluLeuArgArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLys 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     183 GAACTGAGGAGAGCAGTATCTCCCCCTGCCAGAAACATGCTGAAGATGGAATGGAACAAA 242

Qy      81 GluAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSerAsnPro 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     243 GAGGCTGCAGCAAATGCCCAAAAGTGGGCAAACCAGTGCAATTACAGACACAGTAACCCA 302

Qy     101 LysAspArgMetThrSerLeuLysCysGlyGluAsnLeuTyrMetSerSerAlaProSer 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     303 AAGGATCGAATGACAAGTCTAAAATGTGGTGAGAATCTCTACATGTCAAGTGCCCCCAGC 362

Qy     121 SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAspPheAspPheGlyVal 140
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Db     363 TCATGGTCACAAGCAATCCAAAGCTGGTTTGATGAGTACAATGATTTTGACTTTGGTGTA 422

Qy     141 GlyProLysThrProAsnAlaValValGlyHisTyrThrGlnValValTrpTyrSerSer 160
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Db     423 GGGCCAAAGACTCCCAACGCAGTGGTTGGACATTATACACAGGTTGTTTGGTACTCTTCA 482

Qy     161 TyrLeuValGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuLysTyrTyrTyr 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     483 TACCTCGTTGGATGTGGAAATGCCTACTGTCCCAATCAAAAAGTTCTAAAATACTACTAT 542

Qy     181 ValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeuTyrValProTyrGluGln 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     543 GTTTGCCAATATTGTCCTGCTGGTAATTGGGCTAATAGACTATATGTCCCTTATGAACAA 602

Qy     201 GlyAlaProCysAlaSerCysProAspAsnCysAspAspGlyLeuCysThrAsnGlyCys 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     603 GGAGCACCTTGTGCCAGTTGCCCAGATAACTGTGACGATGGACTATGCACCAATGGTTGC 662

Qy     221 LysTyrGluAspLeuTyrSerAsnCysLysSerLeuLysLeuThrLeuThrCysLysHis 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     663 AAGTACGAAGATCTCTATAGTAACTGTAAAAGTTTGAAGCTCACATTAACCTGTAAACAT 722

Qy     241 GlnLeuValArgAspSerCysLysAlaSerCysAsnCysSerAsnSerIleTyr 258
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     723 CAGTTGGTCAGGGACAGTTGCAAGGCATCCTGCAATTGTTCAAACAGCATTTAT 776

RESULT 2
ABV24823
ID   ABV24823 standard; cDNA; 1610 BP.
XX
AC   ABV24823;
XX
DT   16-SEP-2002  (first entry)
XX
DE   Human prostate expression marker cDNA 24814.
XX
KW   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW   pharmacogenomic marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200160860-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US05171.
XX
PR   17-FEB-2000; 2000US-183319P.
PR   16-MAR-2000; 2000US-189862P.
PR   25-MAY-2000; 2000US-207454P.
PR   09-JUN-2000; 2000US-211314P.
PR   18-JUL-2000; 2000US-219007P.
PR   13-DEC-2000; 2000US-255281P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
```

```
PI   Schlegel R,  Endege WO,  Monahan JE;
XX
DR   WPI; 2001-662795/76.
XX
PT   Novel isolated nucleic acid molecule associated with cancerous state of
PT   prostate cells and correlating with presence of prostate cancer, useful
PT   for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS   Claim 1; Page 4758-4759; 11750pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (I) comprising
CC   a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC   specification or its complement. (I) is useful for:
CC   (a) assessing whether a patient is afflicted with prostate cancer;
CC   (b) monitoring the progression of prostate cancer in a patient;
CC   (c) assessing the efficacy of a test compound to inhibit prostate
CC   cancer in a patient;
CC   (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC   in a patient;
CC   (e) selecting a composition for inhibiting prostate cancer in a patient;
CC   (f) assessing the prostate cell carcinogenic potential of a compound;
CC   (g) determining whether prostate cancer has metastasized in a patient;
CC   (h) assessing the aggressiveness or indolence of prostate cancer in a
CC   patient;
CC   (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
XX
SQ   Sequence 1610 BP; 543 A; 292 C; 292 G; 483 T; 0 other;

Alignment Scores:
Pred. No.:              2.45e-136      Length:         1610
Score:                  1433.00        Matches:        257
Percent Similarity:     100.00%        Conservative:   1
Best Local Similarity:  99.61%         Mismatches:     0
Query Match:            99.79%         Indels:         0
DB:                     23             Gaps:           0

US-09-698-781-3 (1-258) x ABV24823 (1-1610)

Qy       1 MetLysGlnIleLeuHisProAlaLeuGluThrThrAlaMetThrLeuProProValLeu 20
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Qy      21 LeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAla 40
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Db     535 TTGTTCCTGGTTGCTGGGCTGCTTCCATCTTTTCCAGCAAATGAAGATAAGGATCCCGCT 594

Qy      41 PheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsn 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     595 TTTACTGCTTTGTTAACCACCCAAACACAAGTGCAAAGGGAGATTGTGAATAAGCACAAT 654

Qy      61 GluLeuArgArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLys 80
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Db     655 GAACTGAGGAGAGCAGTATCTCCCCCTGCCAGAAACATGCTGAAGATGGAATGGAACAAA 714

Qy      81 GluAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSerAsnPro 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     715 GAGGCTGCAGCAAATGCCCAAAAGTGGGCAAACCAGTGCAATTACAGACACAGTAACCCA 774

Qy     101 LysAspArgMetThrSerLeuLysCysGlyGluAsnLeuTyrMetSerSerAlaProSer 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     775 AAGGATCGAATGACAAGTCTAAAATGTGGTGAGAATCTCTACATGTCAAGTGCCCCCAGC 834

Qy     121 SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAspPheAspPheGlyVal 140
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Db     835 TCATGGTCACAAGCAATCCAAAGCTGGTTTGATGAGTACAATGATTTTGACTTTGGTGTA 894

Qy     141 GlyProLysThrProAsnAlaValValGlyHisTyrThrGlnValValTrpTyrSerSer 160
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Db     895 GGGCCAAAGACTCCCAACTCAGTGGTTGGACATTATACACAGGTTGTTTGGTACTCTTCA 954

Qy     161 TyrLeuValGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuLysTyrTyrTyr 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     955 TACCTCGTTGGATGTGGAAATGCCTACTGTCCCAATCAAAAAGTTCTAAAATACTACTAT 1014

Qy     181 ValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeuTyrValProTyrGluGln 200
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Db    1015 GTTTGCCAATATTGTCCTGCTGGTAATTGGGCTAATAGACTATATGTCCCTTATGAACAA 1074

Qy     201 GlyAlaProCysAlaSerCysProAspAsnCysAspAspGlyLeuCysThrAsnGlyCys 220
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Db    1075 GGAGCACCTTGTGCCAGTTGCCCAGATAACTGTGACGATGGACTATGCACCAATGGTTGC 1134

Qy     221 LysTyrGluAspLeuTyrSerAsnCysLysSerLeuLysLeuThrLeuThrCysLysHis 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1135 AAGTACGAAGATCTCTATAGTAACTGTAAAAGTTTGAAGCTCACATTAACCTGTAAACAT 1194

Qy     241 GlnLeuValArgAspSerCysLysAlaSerCysAsnCysSerAsnSerIleTyr 258
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 3
AAH98651
ID   AAH98651 standard; cDNA; 2133 BP.
XX
AC   AAH98651;
XX
DT   12-OCT-2001  (first entry)
XX
DE   Human EST-derived coding sequence SEQ ID NO: 508.
XX
KW   Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW   tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW   diagnostics; forensic test; gene mapping; genetic disorder;
KW   biodiversity; gene therapy; nutrition; ss.
XX
OS   Homo sapiens.
XX
PN   WO200154477-A2.
XX
PD   02-AUG-2001.
XX
PF   25-JAN-2001; 2001WO-US02687.
XX
PR   25-JAN-2000; 2000US-0491404.
PR   17-JUL-2000; 2000US-0617746.
PR   03-AUG-2000; 2000US-0631451.
PR   15-SEP-2000; 2000US-0663870.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Zhou P,  Qian XB,  Wang Z,  Chen R,  Asundi V;
PI   Cao Y,  Drmanac RA,  Zhang J,  Werhman T;
XX
DR   WPI; 2001-476164/51.
DR   P-PSDB; AAM23992.
XX
PT   Isolated polypeptide for treatment of diseases, diagnostics, raising
PT   antibodies and research use -
XX
PS   Claim 1; Page 533; 1275pp; English.
XX
CC   The present invention provides the protein and coding sequences of novel
CC   proteins from a variety of organisms, including human, dog, cat, horse,
CC   cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC   urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC   from the organism of interest. They can be used in diagnostics,
CC   forensics, gene mapping, identification of mutations, to assess
CC   biodiversity and for nutritional purposes. The present sequence is a cDNA
CC   of the invention.
XX
SQ   Sequence 2133 BP; 725 A; 403 C; 382 G; 623 T; 0 other;

Alignment Scores:
Pred. No.:              1.17e-135      Length:         2133
Score:                  1428.00        Matches:        257
Percent Similarity:     99.61%         Conservative:   0
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Best Local Similarity:  99.61%        Mismatches:    1
Query Match:            99.44%        Indels:        0
DB:                     22            Gaps:          0

US-09-698-781-3 (1-258) x AAH98651 (1-2133)

Qy       1 MetLysGlnIleLeuHisProAlaLeuGluThrThrAlaMetThrLeuProValLeu 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 ATGAAACAAATACTTCATCCTGCTCTGGAAACCACTGCAATGACATTATTCCCAGTGCTG 61

Qy      21 LeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAla 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 TTGTTCCTGGTTGCTGGGCTGCTTCCATCTTTTCCAGCAAATGAAGATAAGGATCCCGCT 121

Qy      41 PheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsn 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     122 TTTACTGCTTTGTTAACCACCCAAACACAAGTGCAAAGGGAGATTGTGAATAAGCACAAT 181

Qy      61 GluLeuArgArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLys 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     182 GAACTGAGGAGAGCAGTATCTCCCCCTGCCAGAAACATGCTGAAGATGGAATGGAACAAA 241

Qy      81 GluAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSerAsnPro 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     242 GAGGCTGCAGCAAATGCCCAAAAGTGGGCAAACCAGTGCAATTACAGACACAGTAACCCA 301

Qy     101 LysAspArgMetThrSerLeuLysCysGlyGluAsnLeuTyrMetSerSerAlaProSer 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db     302 AAGGATCGAATGACAAGTCTAAAATGTGGTGAGAATCTCTACATGTCAAGTGCCTCCAGC 361

Qy     121 SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAspPheAspPheGlyVal 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     362 TCATGGTCACAAGCAATCCAAAGCTGGTTTGATGAGTACAATGATTTTGACTTTGGTGTA 421

Qy     141 GlyProLysThrProAsnAlaValValGlyHisTyrThrGlnValValTrpTyrSerSer 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     422 GGGCCAAAGACTCCCAACGCAGTGGTTGGACATTATACACAGGTTGTTTGGTACTCTTCA 481

Qy     161 TyrLeuValGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuLysTyrTyrTyr 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     482 TACCTCGTTGGATGTGGAAATGCCTACTGTCCCAATCAAAAAGTTCTAAAATACTACTAT 541

Qy     181 ValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeuTyrValProTyrGluGln 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     542 GTTTGCCAATATTGTCCTGCTGGTAATTGGGCTAATAGACTATATGTCCCTTATGAACAA 601

Qy     201 GlyAlaProCysAlaSerCysProAspAsnCysAspAspGlyLeuCysThrAsnGlyCys 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     602 GGAGCACCTTGTGCCAGTTGCCCAGATAACTGTGACGATGGACTATGCACCAATGGTTGC 661

Qy     221 LysTyrGluAspLeuTyrSerAsnCysLysSerLeuLysLeuThrLeuThrCysLysHis 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     662 AAGTACGAAGATCTCTATAGTAACTGTAAAAGTTTGAAGCTCACATTAACCTGTAAACAT 721

Qy     241 GlnLeuValArgAspSerCysLysAlaSerCysAsnCysSerAsnSerIleTyr 258
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     722 CAGTTGGTCAGGGACAGTTGCAAGGCATCCTGCAATTGTTCAAACAGCATTTAT 775

RESULT 4
AAH98659
ID   AAH98659 standard; cDNA; 2133 BP.
XX
AC   AAH98659;
XX
DT   12-OCT-2001  (first entry)
XX
DE   Human EST-derived coding sequence SEQ ID NO: 516.
XX
KW   Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW   tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW   diagnostics; forensic test; gene mapping; genetic disorder;
KW   biodiversity; gene therapy; nutrition; ss.
XX
OS   Homo sapiens.
XX
PN   WO200154477-A2.
XX
PD   02-AUG-2001.
XX
PF   25-JAN-2001; 2001WO-US02687.
XX
PR   25-JAN-2000; 2000US-0491404.
PR   17-JUL-2000; 2000US-0617746.
PR   03-AUG-2000; 2000US-0631451.
PR   15-SEP-2000; 2000US-0663870.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Zhou P,  Qian XB,  Wang Z,  Chen R,  Asundi V;
PI   Cao Y,  Drmanac RA,  Zhang J,  Werhman T;
XX
DR   WPI; 2001-476164/51.
DR   P-PSDB; AAM24000.
XX
PT   Isolated polypeptide for treatment of diseases, diagnostics, raising
PT   antibodies and research use -
XX
PS   Claim 1; Page 537-538; 1275pp; English.
XX
CC   The present invention provides the protein and coding sequences of novel
CC   proteins from a variety of organisms, including human, dog, cat, horse,
CC   cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC   urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC   from the organism of interest. They can be used in diagnostics,
CC   forensics, gene mapping, identification of mutations, to assess
CC   biodiversity and for nutritional purposes. The present sequence is a cDNA
CC   of the invention.
XX
SQ   Sequence 2133 BP; 725 A; 403 C; 382 G; 623 T; 0 other;

Alignment Scores:
Pred. No.:              1.17e-135       Length:         2133
Score:                  1428.00         Matches:        257
Percent Similarity:     99.61%          Conservative:   0
Best Local Similarity:  99.61%          Mismatches:     1
Query Match:            99.44%          Indels:         0
DB:                     22              Gaps:           0

US-09-698-781-3 (1-258) x AAH98659 (1-2133)

Qy       1 MetLysGlnIleLeuHisProAlaLeuGluThrThrAlaMetThrLeuProValLeu 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 ATGAAACAAATACTTCATCCTGCTCTGGAAACCACTGCAATGACATTATTCCCAGTGCTG 61

Qy      21 LeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAla 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 TTGTTCCTGGTTGCTGGGCTGCTTCCATCTTTTCCAGCAAATGAAGATAAGGATCCCGCT 121

Qy      41 PheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsn 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     122 TTTACTGCTTTGTTAACCACCCAAACACAAGTGCAAAGGGAGATTGTGAATAAGCACAAT 181

Qy      61 GluLeuArgArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLys 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     182 GAACTGAGGAGAGCAGTATCTCCCCCTGCCAGAAACATGCTGAAGATGGAATGGAACAAA 241

Qy      81 GluAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSerAsnPro 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     242 GAGGCTGCAGCAAATGCCCAAAAGTGGGCAAACCAGTGCAATTACAGACACAGTAACCCA 301

Qy     101 LysAspArgMetThrSerLeuLysCysGlyGluAsnLeuTyrMetSerSerAlaProSer 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db     302 AAGGATCGAATGACAAGTCTAAAATGTGGTGAGAATCTCTACATGTCAAGTGCCTCCAGC 361

Qy     121 SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAspPheAspPheGlyVal 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    362 TCATGGTCACAAGCAATCCAAAGCTGGTTTGATGAGTACAATGATTTTGACTTTGGTGTA 421

Qy    141 GlyProLysThrProAsnAlaValValGlyHisTyrThrGlnValValTrpTyrSerSer 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    422 GGGCCAAAGACTCCCAACGCAGTGGTTGGACATTATACACAGGTTGTTTGGTACTCTTCA 481

Qy    161 TyrLeuValGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuLysTyrTyrTyr 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    482 TACCTCGTTGGATGTGGAAATGCCTACTGTCCCAATCAAAAAGTTCTAAAATACTACTAT 541

Qy    181 ValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeuTyrValProTyrGluGln 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    542 GTTTGCCAATATTGTCCTGCTGGTAATTGGGCTAATAGACTATATGTCCCTTATGAACAA 601

Qy    201 GlyAlaProCysAlaSerCysProAspAsnCysAspAspGlyLeuCysThrAsnGlyCys 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    602 GGAGCACCTTGTGCCAGTTGCCCAGATAACTGTGACGATGGACTATGCACCAATGGTTGC 661

Qy    221 LysTyrGluAspLeuTyrSerAsnCysLysSerLeuLysLeuThrLeuThrCysLysHis 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    662 AAGTACGAAGATCTCTATAGTAACTGTAAAAGTTTGAAGCTCACATTAACCTGTAAACAT 721

Qy    241 GlnLeuValArgAspSerCysLysAlaSerCysAsnCysSerAsnSerIleTyr 258
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    722 CAGTTGGTCAGGGACAGTTGCAAGGCATCCTGCAATTGTTCAAACAGCATTTAT 775

RESULT 5
ABV22644
ID   ABV22644 standard; cDNA; 2452 BP.
XX
AC   ABV22644;
XX
DT   13-SEP-2002  (first entry)
XX
DE   Human prostate expression marker cDNA 22635.
XX
KW   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW   pharmacogenomic marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200160860-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US05171.
XX
PR   17-FEB-2000; 2000US-183319P.
PR   16-MAR-2000; 2000US-189862P.
PR   25-MAY-2000; 2000US-207454P.
PR   09-JUN-2000; 2000US-211314P.
PR   18-JUL-2000; 2000US-219007P.
PR   13-DEC-2000; 2000US-255281P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Endege WO,  Monahan JE;
XX
DR   WPI; 2001-662795/76.
XX
PT   Novel isolated nucleic acid molecule associated with cancerous state of
PT   prostate cells and correlating with presence of prostate cancer, useful
PT   for detecting presence of prostate cancer, stage of prostate cancer
XX
PS   Claim 1; Page 3969-3970; 11750pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (I) comprising
CC   a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC   specification or its complement. (I) is useful for:
CC   (a) assessing whether a patient is afflicted with prostate cancer;
CC   (b) monitoring the progression of prostate cancer in a patient;
CC   (c) assessing the efficacy of a test compound to inhibit prostate
CC   cancer in a patient;
CC   (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC   in a patient;
CC   (e) selecting a composition for inhibiting prostate cancer in a patient;
CC   (f) assessing the prostate cell carcinogenic potential of a compound;
CC   (g) determining whether prostate cancer has metastasized in a patient;
CC   (h) assessing the aggressiveness or indolence of prostate cancer in a
CC   patient;
CC   (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
XX
SQ   Sequence 2452 BP; 787 A; 467 C; 444 G; 754 T; 0 other;

Alignment Scores:
Pred. No.:              1.43e-135      Length:          2452
Score:                  1428.00        Matches:         257
Percent Similarity:     99.61%         Conservative:    0
Best Local Similarity:  99.61%         Mismatches:      1
Query Match:            99.44%         Indels:          0
DB:                     23             Gaps:            0

US-09-698-781-3 (1-258) x ABV22644 (1-2452)

Qy      1 MetLysGlnIleLeuHisProAlaLeuGluThrThrAlaMetThrLeuProProValLeu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    197 ATGAAACAAATACTTCATCCTGCTCTGGAAACCACTGCAATGACATTATTCCCAGTGCTG 256

Qy     21 LeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAla 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    257 TTGTTCCTGGTTGCTGGGCTGCTTCCATCTTTTCCAGCAAATGAAGATAAGGATCCCGCT 316

Qy     41 PheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsn 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    317 TTTACTGCTTTGTTAACCACCCAAACACAAGTGCAAAGGGAGATTGTGAATAAGCACAAT 376

Qy     61 GluLeuArgArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLys 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    377 GAACTGAGGAGAGCAGTATCTCCCCCTGCCAGAAACATGCTGAAGATGGAATGGAACAAA 436

Qy     81 GluAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSerAsnPro 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    437 GAGGCTGCAGCAAATGCCCAAAAGTGGGCAAACCAGTGCAATTACAGACACAGTAACCCA 496

Qy    101 LysAspArgMetThrSerLeuLysCysGlyGluAsnLeuTyrMetSerSerAlaProSer 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db    497 AAGGATCGAATGACAAGTCTAAAATGTGGTGAGAATCTCTACATGTCAAGTGCCTCCAGC 556

Qy    121 SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAspPheAspPheGlyVal 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    557 TCATGGTCACAAGCAATCCAAAGCTGGTTTGATGAGTACAATGATTTTGACTTTGGTGTA 616

Qy    141 GlyProLysThrProAsnAlaValValGlyHisTyrThrGlnValValTrpTyrSerSer 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    617 GGGCCAAAGACTCCCAACGCAGTGGTTGGACATTATACACAGGTTGTTTGGTACTCTTCA 676

Qy    161 TyrLeuValGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuLysTyrTyrTyr 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    677 TACCTCGTTGGATGTGGAAATGCCTACTGTCCCAATCAAAAAGTTCTAAAATACTACTAT 736

Qy    181 ValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeuTyrValProTyrGluGln 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    737 GTTTGCCAATATTGTCCTGCTGGTAATTGGGCTAATAGACTATATGTCCCTTATGAACAA 796

Qy    201 GlyAlaProCysAlaSerCysProAspAsnCysAspAspGlyLeuCysThrAsnGlyCys 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    797 GGAGCACCTTGTGCCAGTTGCCCAGATAACTGTGACGATGGACTATGCACCAATGGTTGC 856

Qy    221 LysTyrGluAspLeuTyrSerAsnCysLysSerLeuLysLeuThrLeuThrCysLysHis 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    857 AAGTACGAAGATCTCTATAGTAACTGTAAAAGTTTGAAGCTCACATTAACCTGTAAACAT 916

Qy    241 GlnLeuValArgAspSerCysLysAlaSerCysAsnCysSerAsnSerIleTyr 258
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    917 CAGTTGGTCAGGGACAGTTGCAAGGCCTCCTGCAATTGTTCAAACAGCATTTAT 970
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RESULT 6
ABV24631
ID   ABV24631 standard; cDNA; 2452 BP.
XX
AC   ABV24631;
XX
DT   16-SEP-2002  (first entry)
XX
DE   Human prostate expression marker cDNA 24622.
XX
KW   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW   pharmacogenomic marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200160860-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US05171.
XX
PR   17-FEB-2000; 2000US-183319P.
PR   16-MAR-2000; 2000US-189862P.
PR   25-MAY-2000; 2000US-207454P.
PR   09-JUN-2000; 2000US-211314P.
PR   18-JUL-2000; 2000US-219007P.
PR   13-DEC-2000; 2000US-255281P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Endege WO,. Monahan JE;
XX
DR   WPI; 2001-662795/76.
XX
PT   Novel isolated nucleic acid molecule associated with cancerous state of
PT   prostate cells and correlating with presence of prostate cancer, useful
PT   for detecting presence of prostate cancer, stage of prostate cancer  -
XX
PS   Claim 1; Page 4680-4681; 11750pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (I) comprising
CC   a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC   specification or its complement. (I) is useful for:
CC   (a) assessing whether a patient is afflicted with prostate cancer;
CC   (b) monitoring the progression of prostate cancer in a patient;
CC   (c) assessing the efficacy of a test compound to inhibit prostate
CC   cancer in a patient;
CC   (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC   in a patient;
CC   (e) selecting a composition for inhibiting prostate cancer in a patient;
CC   (f) assessing the prostate cell carcinogenic potential of a compound;
CC   (g) determining whether prostate cancer has metastasized in a patient;
CC   (h) assessing the aggressiveness or indolence of prostate cancer in a
CC   patient;
CC   (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
XX
SQ   Sequence 2452 BP; 787 A; 467 C; 444 G; 754 T; 0 other;

Alignment Scores:
Pred. No.:                1.43e-135      Length:          2452
Score:                    1428.00        Matches:         257
Percent Similarity:       99.61%         Conservative:    0
Best Local Similarity:    99.61%         Mismatches:      1
Query Match:              99.44%         Indels:          0
DB:                       23             Gaps:            0

US-09-698-781-3 (1-258) x ABV24631 (1-2452)

Qy       1 MetLysGlnIleLeuHisProAlaLeuGluThrThrAlaMetThrLeuProValLeu 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     197 ATGAAACAAATACTTCATCCTGCTCTGGAAACCACTGCAATGACATTATTCCCAGTGCTG 256

Qy      21 LeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAla 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     257 TTGTTCCTGGTTGCTGGGCTGCTTCCATCTTTTCCAGCAAATGAAGATAAGGATCCCGCT 316

Qy      41 PheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsn 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     317 TTTACTGCTTTGTTAACCACCCAAACACAAGTGCAAAGGGAGATTGTGAATAAGCACAAT 376

Qy      61 GluLeuArgArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLys 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     377 GAACTGAGGAGAGCAGTATCTCCCCCTGCCAGAAACATGCTGAAGATGGAATGGAACAAA 436

Qy      81 GluAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSerAsnPro 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     437 GAGGCTGCAGCAAATGCCCAAAAGTGGGCAAACCAGTGCAATTACAGACACAGTAACCCA 496

Qy     101 LysAspArgMetThrSerLeuLysCysGlyGluAsnLeuTyrMetSerSerAlaProSer 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||||
Db     497 AAGGATCGAATGACAAGTCTAAAATGTGGTGAGAATCTCTACATGTCAAGTGCCTCCAGC 556

Qy     121 SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAspPheAspPheGlyVal 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     557 TCATGGTCACAAGCAATCCAAAGCTGGTTTGATGAGTACAATGATTTTGACTTTGGTGTA 616

Qy     141 GlyProLysThrProAsnAlaValValGlyHisTyrThrGlnValValTrpTyrSerSer 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     617 GGGCCAAAGACTCCCAACGCAGTGGTTGGACATTATACACAGGTTGTTTGGTACTCTTCA 676

Qy     161 TyrLeuValGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuLysTyrTyrTyr 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     677 TACCTCGTTGGATGTGGAAATGCCTACTGTCCCAATCAAAAAGTTCTAAAATACTACTAT 736

Qy     181 ValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeuTyrValProTyrGluGln 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     737 GTTTGCCAATATTGTCCTGCTGGTAATTGGGCTAATAGACTATATGTCCCTTATGAACAA 796

Qy     201 GlyAlaProCysAlaSerCysProAspAsnCysAspAspGlyLeuCysThrAsnGlyCys 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     797 GGAGCACCTTGTGCCAGTTGCCCAGATAACTGTGACGATGGACTATGCACCAATGGTTGC 856

Qy     221 LysTyrGluAspLeuTyrSerAsnCysLysSerLeuLysLeuThrLeuThrCysLysHis 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     857 AAGTACGAAGATCTCTATAGTAACTGTAAAAGTTTGAAGCTCACATTAACCTGTAAACAT 916

Qy     241 GlnLeuValArgAspSerCysLysAlaSerCysAsnCysSerAsnSerIleTyr 258
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     917 CAGTTGGTCAGGGACAGTTGCAAGGCCTCCTGCAATTGTTCAAACAGCATTTAT 970

RESULT 7
ABV25272
ID   ABV25272 standard; cDNA; 2452 BP.
XX
AC   ABV25272;
XX
DT   16-SEP-2002  (first entry)
XX
DE   Human prostate expression marker cDNA 25263.
XX
KW   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW   pharmacogenomic marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200160860-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US05171.
XX
PR   17-FEB-2000; 2000US-183319P.
PR   16-MAR-2000; 2000US-189862P.
PR   25-MAY-2000; 2000US-207454P.
PR   09-JUN-2000; 2000US-211314P.
PR   18-JUL-2000; 2000US-219007P.
```

```
PR   13-DEC-2000; 2000US-255281P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Endege WO,  Monahan JE;
XX
DR   WPI; 2001-662795/76.
XX
PT   Novel isolated nucleic acid molecule associated with cancerous state of
PT   prostate cells and correlating with presence of prostate cancer, useful
PT   for detecting presence of prostate cancer, stage of prostate cancer  -
XX
PS   Claim 1; Page 4961; 11750pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (I) comprising
CC   a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC   specification or its complement. (I) is useful for:
CC   (a) assessing whether a patient is afflicted with prostate cancer;
CC   (b) monitoring the progression of prostate cancer in a patient;
CC   (c) assessing the efficacy of a test compound to inhibit prostate
CC   cancer in a patient;
CC   (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC   in a patient;
CC   (e) selecting a composition for inhibiting prostate cancer in a patient;
CC   (f) assessing the prostate cell carcinogenic potential of a compound;
CC   (g) determining whether prostate cancer has metastasized in a patient;
CC   (h) assessing the aggressiveness or indolence of prostate cancer in a
CC   patient;
CC   (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
XX
SQ   Sequence 2452 BP; 787 A; 467 C; 444 G; 754 T; 0 other;

Alignment Scores:
Pred. No.:              1.43e-135       Length:         2452
Score:                  1428.00         Matches:        257
Percent Similarity:     99.61%          Conservative:   0
Best Local Similarity:  99.61%          Mismatches:     1
Query Match:            99.44%          Indels:         0
DB:                     23              Gaps:           0

US-09-698-781-3 (1-258) x ABV25272 (1-2452)

Qy       1 MetLysGlnIleLeuHisProAlaLeuGluThrThrAlaMetThrLeuPheProValLeu 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     197 ATGAAACAAATACTTCATCCTGCTCTGGAAACCACTGCAATGACATTATTCCCAGTGCTG 256

Qy      21 LeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAla 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     257 TTGTTCCTGGTTGCTGGGCTGCTTCCATCTTTTCCAGCAAATGAAGATAAGGATCCCGCT 316

Qy      41 PheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsn 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     317 TTTACTGCTTTGTTAACCACCCAAACACAAGTGCAAAGGGAGATTGTGAATAAGCACAAT 376

Qy      61 GluLeuArgArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLys 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     377 GAACTGAGGAGAGCAGTATCTCCCCCTGCCAGAAACATGCTGAAGATGGAATGGAACAAA 436

Qy      81 GluAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSerAsnPro 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     437 GAGGCTGCAGCAAATGCCCAAAAGTGGGCAAACCAGTGCAATTACAGACACAGTAACCCA 496

Qy     101 LysAspArgMetThrSerLeuLysCysGlyGluAsnLeuTyrMetSerSerAlaProSer 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db     497 AAGGATCGAATGACAAGTCTAAAATGTGGTGAGAATCTCTACATGTCAAGTGCCTCCAGC 556

Qy     121 SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAspPheAspPheGlyVal 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     557 TCATGGTCACAAGCAATCCAAAGCTGGTTTGATGAGTACAATGATTTTGACTTTGGTGTA 616

Qy     141 GlyProLysThrProAsnAlaValValGlyHisTyrThrGlnValValTrpTyrSerSer 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     617 GGGCCAAAGACTCCCAACGCAGTGGTTGGACATTATACACAGGTTGTTTGGTACTCTTCA 676

Qy     161 TyrLeuValGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuLysTyrTyrTyr 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     677 TACCTCGTTGGATGTGGAAATGCCTACTGTCCCAATCAAAAAGTTCTAAAATACTACTAT 736

Qy     181 ValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeuTyrValProTyrGluGln 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     737 GTTTGCCAATATTGTCCTGCTGGTAATTGGGCTAATAGACTATATGTCCCTTATGAACAA 796

Qy     201 GlyAlaProCysAlaSerCysProAspAsnCysAspAspGlyLeuCysThrAsnGlyCys 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     797 GGAGCACCTTGTGCCAGTTGCCCAGATAACTGTGACGATGGACTATGCACCAATGGTTGC 856

Qy     221 LysTyrGluAspLeuTyrSerAsnCysLysSerLeuLysLeuThrLeuThrCysLysHis 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     857 AAGTACGAAGATCTCTATAGTAACTGTAAAAGTTTGAAGCTCACATTAACCTGTAAACAT 916

Qy     241 GlnLeuValArgAspSerCysLysAlaSerCysAsnCysSerAsnSerIleTyr 258
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     917 CAGTTGGTCAGGGACAGTTGCAAGGCCTCCTGCAATTGTTCAAACAGCATTTAT 970

RESULT 8
ABV25706
ID   ABV25706 standard; cDNA; 2452 BP.
XX
AC   ABV25706;
XX
DT   16-SEP-2002  (first entry)
XX
DE   Human prostate expression marker cDNA 25697.
XX
KW   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW   pharmacogenomic marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200160860-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US05171.
XX
PR   17-FEB-2000; 2000US-183319P.
PR   16-MAR-2000; 2000US-189862P.
PR   25-MAY-2000; 2000US-207454P.
PR   09-JUN-2000; 2000US-211314P.
PR   18-JUL-2000; 2000US-219007P.
PR   13-DEC-2000; 2000US-255281P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Endege WO,  Monahan JE;
XX
DR   WPI; 2001-662795/76.
XX
PT   Novel isolated nucleic acid molecule associated with cancerous state of
PT   prostate cells and correlating with presence of prostate cancer, useful
PT   for detecting presence of prostate cancer, stage of prostate cancer  -
XX
PS   Claim 1; Page 5156-5157; 11750pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (I) comprising
CC   a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC   specification or its complement. (I) is useful for:
CC   (a) assessing whether a patient is afflicted with prostate cancer;
CC   (b) monitoring the progression of prostate cancer in a patient;
CC   (c) assessing the efficacy of a test compound to inhibit prostate
CC   cancer in a patient;
CC   (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC   in a patient;
CC   (e) selecting a composition for inhibiting prostate cancer in a patient;
CC   (f) assessing the prostate cell carcinogenic potential of a compound;
CC   (g) determining whether prostate cancer has metastasized in a patient;
```

```
CC   (h) assessing the aggressiveness or indolence of prostate cancer in a
CC   patient;
CC   (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
XX
SQ   Sequence 2452 BP; 787 A; 467 C; 444 G; 754 T; 0 other;

Alignment Scores:
Pred. No.:              1.43e-135      Length:         2452
Score:                  1428.00        Matches:        257
Percent Similarity:     99.61%         Conservative:   0
Best Local Similarity:  99.61%         Mismatches:     1
Query Match:            99.44%         Indels:         0
DB:                     23             Gaps:           0

US-09-698-781-3 (1-258) x ABV25706 (1-2452)

Qy       1 MetLysGlnIleLeuHisProAlaLeuGluThrThrAlaMetThrLeuPheProValLeu 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     197 ATGAAACAAATACTTCATCCTGCTCTGGAAACCACTGCAATGACATTATTCCCAGTGCTG 256

Qy      21 LeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAla 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     257 TTGTTCCTGGTTGCTGGGCTGCTTCCATCTTTTCCAGCAAATGAAGATAAGGATCCCGCT 316

Qy      41 PheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsn 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     317 TTTACTGCTTTGTTAACCACCCAAACACAAGTGCAAAGGGAGATTGTGAATAAGCACAAT 376

Qy      61 GluLeuArgArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLys 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     377 GAACTGAGGAGAGCAGTATCTCCCCCTGCCAGAAACATGCTGAAGATGGAATGGAACAAA 436

Qy      81 GluAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSerAsnPro 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     437 GAGGCTGCAGCAAATGCCCAAAAGTGGGCAAACCAGTGCAATTACAGACACAGTAACCCA 496

Qy     101 LysAspArgMetThrSerLeuLysCysGlyGluAsnLeuTyrMetSerSerAlaProSer 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||||||
Db     497 AAGGATCGAATGACAAGTCTAAAATGTGGTGAGAATCTCTACATGTCAAGTGCCTCCAGC 556

Qy     121 SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAspPheAspPheGlyVal 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     557 TCATGGTCACAAGCAATCCAAAGCTGGTTTGATGAGTACAATGATTTTGACTTTGGTGTA 616

Qy     141 GlyProLysThrProAsnAlaValValGlyHisTyrThrGlnValValTrpTyrSerSer 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     617 GGGCCAAAGACTCCCAACGCAGTGGTTGGACATTATACACAGGTTGTTTGGTACTCTTCA 676

Qy     161 TyrLeuValGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuLysTyrTyrTyr 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     677 TACCTCGTTGGATGTGGAAATGCCTACTGTCCCAATCAAAAAGTTCTAAAATACTACTAT 736

Qy     181 ValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeuTyrValProTyrGluGln 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     737 GTTTGCCAATATTGTCCTGCTGGTAATTGGGCTAATAGACTATATGTCCCTTATGAACAA 796

Qy     201 GlyAlaProCysAlaSerCysProAspAsnCysAspAspGlyLeuCysThrAsnGlyCys 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     797 GGAGCACCTTGTGCCAGTTGCCCAGATAACTGTGACGATGGACTATGCACCAATGGTTGC 856

Qy     221 LysTyrGluAspLeuTyrSerAsnCysLysSerLeuLysLeuThrLeuThrCysLysHis 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     857 AAGTACGAAGATCTCTATAGTAACTGTAAAAGTTTGAAGCTCACATTAACCTGTAAACAT 916

Qy     241 GlnLeuValArgAspSerCysLysAlaSerCysAsnCysSerAsnSerIleTyr 258
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     917 CAGTTGGTCAGGGACAGTTGCAAGGCCTCCTGCAATTGTTCAAACAGCATTTAT 970

RESULT 9
ABV28467
ID   ABV28467 standard; cDNA; 2452 BP.
XX
AC   ABV28467;
XX
DT   16-SEP-2002  (first entry)
XX
DE   Human prostate expression marker cDNA 28458.
XX
KW   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW   pharmacogenomic marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200160860-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US05171.
XX
PR   17-FEB-2000; 2000US-183319P.
PR   16-MAR-2000; 2000US-189862P.
PR   25-MAY-2000; 2000US-207454P.
PR   09-JUN-2000; 2000US-211314P.
PR   18-JUL-2000; 2000US-219007P.
PR   13-DEC-2000; 2000US-255281P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Endege WO,  Monahan JE;
XX
DR   WPI; 2001-662795/76.
XX
PT   Novel isolated nucleic acid molecule associated with cancerous state of
PT   prostate cells and correlating with presence of prostate cancer, useful
PT   for detecting presence of prostate cancer, stage of prostate cancer  -
XX
PS   Claim 1; Page 5942-5943; 11750pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (I) comprising
CC   a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC   specification or its complement. (I) is useful for:
CC   (a) assessing whether a patient is afflicted with prostate cancer;
CC   (b) monitoring the progression of prostate cancer in a patient;
CC   (c) assessing the efficacy of a test compound to inhibit prostate
CC   cancer in a patient;
CC   (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC   in a patient;
CC   (e) selecting a composition for inhibiting prostate cancer in a patient;
CC   (f) assessing the prostate cell carcinogenic potential of a compound;
CC   (g) determining whether prostate cancer has metastasized in a patient;
CC   (h) assessing the aggressiveness or indolence of prostate cancer in a
CC   patient;
CC   (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
XX
SQ   Sequence 2452 BP; 787 A; 467 C; 444 G; 754 T; 0 other;

Alignment Scores:
Pred. No.:              1.43e-135      Length:         2452
Score:                  1428.00        Matches:        257
Percent Similarity:     99.61%         Conservative:   0
Best Local Similarity:  99.61%         Mismatches:     1
Query Match:            99.44%         Indels:         0
DB:                     23             Gaps:           0

US-09-698-781-3 (1-258) x ABV28467 (1-2452)

Qy       1 MetLysGlnIleLeuHisProAlaLeuGluThrThrAlaMetThrLeuPheProValLeu 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     197 ATGAAACAAATACTTCATCCTGCTCTGGAAACCACTGCAATGACATTATTCCCAGTGCTG 256

Qy      21 LeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAla 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     257 TTGTTCCTGGTTGCTGGGCTGCTTCCATCTTTTCCAGCAAATGAAGATAAGGATCCCGCT 316

Qy      41 PheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsn 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    317 TTTACTGCTTTGTTAACCACCCAAACACAAGTGCAAAGGGAGATTGTGAATAAGCACAAT 376

Qy     61 GluLeuArgArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLys 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    377 GAACTGAGGAGAGCAGTATCTCCCCCTGCCAGAAACATGCTGAAGATGGAATGGAACAAA 436

Qy     81 GluAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSerAsnPro 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    437 GAGGCTGCAGCAAATGCCCAAAAGTGGGCAAACCAGTGCAATTACAGACACAGTAACCCA 496

Qy    101 LysAspArgMetThrSerLeuLysCysGlyGluAsnLeuTyrMetSerSerAlaProSer 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db    497 AAGGATCGAATGACAAGTCTAAAATGTGGTGAGAATCTCTACATGTCAAGTGCCTCCAGC 556

Qy    121 SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAspPheAspPheGlyVal 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    557 TCATGGTCACAAGCAATCCAAAGCTGGTTTGATGAGTACAATGATTTTGACTTTGGTGTA 616

Qy    141 GlyProLysThrProAsnAlaValValGlyHisTyrThrGlnValValTrpTyrSerSer 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    617 GGGCCAAAGACTCCCAACGCAGTGGTTGGACATTATACACAGGTTGTTTGGTACTCTTCA 676

Qy    161 TyrLeuValGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuLysTyrTyrTyr 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    677 TACCTCGTTGGATGTGGAAATGCCTACTGTCCCAATCAAAAAGTTCTAAAATACTACTAT 736

Qy    181 ValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeuTyrValProTyrGluGln 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    737 GTTTGCCAATATTGTCCTGCTGGTAATTGGGCTAATAGACTATATGTCCCTTATGAACAA 796

Qy    201 GlyAlaProCysAlaSerCysProAspAsnCysAspAspGlyLeuCysThrAsnGlyCys 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    797 GGAGCACCTTGTGCCAGTTGCCCAGATAACTGTGACGATGGACTATGCACCAATGGTTGC 856

Qy    221 LysTyrGluAspLeuTyrSerAsnCysLysSerLeuLysLeuThrLeuThrCysLysHis 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    857 AAGTACGAAGATCTCTATAGTAACTGTAAAAGTTTGAAGCTCACATTAACCTGTAAACAT 916

Qy    241 GlnLeuValArgAspSerCysLysAlaSerCysAsnCysSerAsnSerIleTyr 258
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    917 CAGTTGGTCAGGGACAGTTGCAAGGCCTCCTGCAATTGTTCAAACAGCATTTAT 970

RESULT 10
ABV28648
ID   ABV28648 standard; cDNA; 2452 BP.
XX
AC   ABV28648;
XX
DT   16-SEP-2002  (first entry)
XX
DE   Human prostate expression marker cDNA 28639.
XX
KW   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW   pharmacogenomic marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200160860-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US05171.
XX
PR   17-FEB-2000; 2000US-183319P.
PR   16-MAR-2000; 2000US-189862P.
PR   25-MAY-2000; 2000US-207454P.
PR   09-JUN-2000; 2000US-211314P.
PR   18-JUL-2000; 2000US-219007P.
PR   13-DEC-2000; 2000US-255281P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Endege WO,  Monahan JE;
XX
DR   WPI; 2001-662795/76.
XX
PT   Novel isolated nucleic acid molecule associated with cancerous state of
PT   prostate cells and correlating with presence of prostate cancer, useful
PT   for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS   Claim 1; Page 6006; 11750pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (I) comprising
CC   a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC   specification or its complement. (I) is useful for:
CC   (a) assessing whether a patient is afflicted with prostate cancer;
CC   (b) monitoring the progression of prostate cancer in a patient;
CC   (c) assessing the efficacy of a test compound to inhibit prostate
CC   cancer in a patient;
CC   (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC   in a patient;
CC   (e) selecting a composition for inhibiting prostate cancer in a patient;
CC   (f) assessing the prostate cell carcinogenic potential of a compound;
CC   (g) determining whether prostate cancer has metastasized in a patient;
CC   (h) assessing the aggressiveness or indolence of prostate cancer in a
CC   patient;
CC   (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
XX
SQ   Sequence 2452 BP; 787 A; 467 C; 444 G; 754 T; 0 other;

Alignment Scores:
Pred. No.:              1.43e-135      Length:          2452
Score:                  1428.00        Matches:         257
Percent Similarity:     99.61%         Conservative:    0
Best Local Similarity:  99.61%         Mismatches:      1
Query Match:            99.44%         Indels:          0
DB:                     23             Gaps:            0

US-09-698-781-3 (1-258) x ABV28648 (1-2452)

Qy      1 MetLysGlnIleLeuHisProAlaLeuGluThrThrAlaMetThrLeuPheProValLeu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    197 ATGAAACAAATACTTCATCCTGCTCTGGAAACCACTGCAATGACATTATTCCCAGTGCTG 256

Qy     21 LeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAla 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    257 TTGTTCCTGGTTGCTGGGCTGCTTCCATCTTTTCCAGCAAATGAAGATAAGGATCCCGCT 316

Qy     41 PheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsn 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    317 TTTACTGCTTTGTTAACCACCCAAACACAAGTGCAAAGGGAGATTGTGAATAAGCACAAT 376

Qy     61 GluLeuArgArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLys 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    377 GAACTGAGGAGAGCAGTATCTCCCCCTGCCAGAAACATGCTGAAGATGGAATGGAACAAA 436

Qy     81 GluAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSerAsnPro 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    437 GAGGCTGCAGCAAATGCCCAAAAGTGGGCAAACCAGTGCAATTACAGACACAGTAACCCA 496

Qy    101 LysAspArgMetThrSerLeuLysCysGlyGluAsnLeuTyrMetSerSerAlaProSer 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db    497 AAGGATCGAATGACAAGTCTAAAATGTGGTGAGAATCTCTACATGTCAAGTGCCTCCAGC 556

Qy    121 SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAspPheAspPheGlyVal 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    557 TCATGGTCACAAGCAATCCAAAGCTGGTTTGATGAGTACAATGATTTTGACTTTGGTGTA 616

Qy    141 GlyProLysThrProAsnAlaValValGlyHisTyrThrGlnValValTrpTyrSerSer 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    617 GGGCCAAAGACTCCCAACGCAGTGGTTGGACATTATACACAGGTTGTTTGGTACTCTTCA 676

Qy    161 TyrLeuValGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuLysTyrTyrTyr 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    677 TACCTCGTTGGATGTGGAAATGCCTACTGTCCCAATCAAAAAGTTCTAAAATACTACTAT 736
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Qy     181 ValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeuTyrValProTyrGluGln 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     737 GTTTGCCAATATTGTCCTGCTGGTAATTGGGCTAATAGACTATATGTCCCTTATGAACAA 796

Qy     201 GlyAlaProCysAlaSerCysProAspAsnCysAspAspGlyLeuCysThrAsnGlyCys 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     797 GGAGCACCTTGTGCCAGTTGCCCAGATAACTGTGACGATGGACTATGCACCAATGGTTGC 856

Qy     221 LysTyrGluAspLeuTyrSerAsnCysLysSerLeuLysLeuThrLeuThrCysLysHis 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     857 AAGTACGAAGATCTCTATAGTAACTGTAAAAGTTTGAAGCTCACATTAACCTGTAAACAT 916

Qy     241 GlnLeuValArgAspSerCysLysAlaSerCysAsnCysSerAsnSerIleTyr 258
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     917 CAGTTGGTCAGGGACAGTTGCAAGGCCTCCTGCAATTGTTCAAACAGCATTTAT 970

RESULT 11
ABL67806
ID   ABL67806 standard; DNA; 2128 BP.
XX
AC   ABL67806;
XX
DT   15-MAY-2002  (first entry)
XX
DE   Oesophagus cancer related gene sequence SEQ ID NO:6143.
XX
KW   Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW   stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW   cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200194629-A2.
XX
PD   13-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-US10838.
XX
PR   05-JUN-2000; 2000US-209473P.
PR   05-JUN-2000; 2000US-209531P.
PR   18-SEP-2000; 2000US-233133P.
PR   18-SEP-2000; 2000US-233617P.
PR   20-SEP-2000; 2000US-234009P.
PR   20-SEP-2000; 2000US-234034P.
PR   20-SEP-2000; 2000US-234052P.
PR   22-SEP-2000; 2000US-234509P.
PR   22-SEP-2000; 2000US-234567P.
PR   25-SEP-2000; 2000US-234923P.
PR   25-SEP-2000; 2000US-234924P.
PR   25-SEP-2000; 2000US-235077P.
PR   25-SEP-2000; 2000US-235082P.
PR   25-SEP-2000; 2000US-235134P.
PR   25-SEP-2000; 2000US-235280P.
PR   26-SEP-2000; 2000US-235637P.
PR   26-SEP-2000; 2000US-235638P.
PR   27-SEP-2000; 2000US-235711P.
PR   27-SEP-2000; 2000US-235720P.
PR   27-SEP-2000; 2000US-235840P.
PR   27-SEP-2000; 2000US-235863P.
PR   28-SEP-2000; 2000US-236028P.
PR   28-SEP-2000; 2000US-236032P.
PR   28-SEP-2000; 2000US-236033P.
PR   28-SEP-2000; 2000US-236034P.
PR   28-SEP-2000; 2000US-236109P.
PR   28-SEP-2000; 2000US-236111P.
PR   29-SEP-2000; 2000US-236842P.
PR   29-SEP-2000; 2000US-236891P.
PR   02-OCT-2000; 2000US-237172P.
PR   02-OCT-2000; 2000US-237173P.
PR   02-OCT-2000; 2000US-237278P.
PR   02-OCT-2000; 2000US-237294P.
PR   02-OCT-2000; 2000US-237295P.
PR   02-OCT-2000; 2000US-237316P.
PR   03-OCT-2000; 2000US-237425P.
PR   03-OCT-2000; 2000US-237598P.
PR   03-OCT-2000; 2000US-237604P.
PR   03-OCT-2000; 2000US-237606P.
PR   03-OCT-2000; 2000US-237608P.
PR   01-NOV-2000; 2000US-244867P.
PR   01-NOV-2000; 2000US-245084P.
XX
PA   (AVAL-) AVALON PHARM.
XX
PI   Young PE,  Augustus M,  Carter KC,  Ebner R,  Endress G,  Horrigan S;
PI   Soppet DR,  Weaver Z;
XX
DR   WPI; 2002-188264/24.
XX
PT   Screening for anti-neoplastic agent involves exposing cells to a
PT   chemical agent to be tested for anti-neoplastic activity, and
PT   determining a change in expression of a gene of a signature gene set
XX
PS   Claim 1; SEQ ID 6143; 44pp; English.
XX
CC   The present invention describes a method (M1) for screening for an
CC   anti-neoplastic agent. The method involves exposing cells to a chemical
CC   agent to be tested for anti-neoplastic activity, determining a change in
CC   expression of at least one gene (I) of a signature gene set, where (I)
CC   comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC   to ABL70110), or is at least 95% identical to (S), where a change in
CC   expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC   activity and can be used in gene therapy. M1 can be used for screening
CC   an anti-neoplastic agent, and can be used for producing a product which
CC   is the data collected with respect to the anti-neoplastic agent as a
CC   result of M1, and the data is sufficient to convey the chemical
CC   structure and/or properties of the agent. M1 can be used in the
CC   treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC   oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC   adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC   infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC   carcinoma, papillary carcinoma and Wilm's tumour.
XX
SQ   Sequence 2128 BP; 734 A; 397 C; 380 G; 617 T; 0 other;

Alignment Scores:
Pred. No.:              2.26e-131      Length:          2128
Score:                  1386.00        Matches:         249
Percent Similarity:     99.60%         Conservative:    0
Best Local Similarity:  99.60%         Mismatches:      1
Query Match:            96.52%         Indels:          0
DB:                     24             Gaps:            0

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Qy       9 LeuGluThrThrAlaMetThrLeuProValLeuLeuPheLeuValAlaGlyLeuLeu 28
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CTGGAAACCACTGCAATGACATTATTCCCAGTGCTGTTGTTCCTGGTTGCTGGGCTGCTT 60

Qy      29 ProSerPheProAlaAsnGluAspLysAspProAlaPheThrAlaLeuLeuThrThrGln 48
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CCATCTTTTCCAGCAAATGAAGATAAGGATCCCGCTTTTACTGCTTTGTTAACCACCCAA 120

Qy      49 ThrGlnValGlnArgGluIleValAsnLysHisAsnGluLeuArgArgAlaValSerPro 68
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ACACAAGTGCAAAGGGAGATTGTGAATAAGCACAATGAACTGAGGAGAGCAGTATCTCCC 180

Qy      69 ProAlaArgAsnMetLeuLysMetGluTrpAsnLysGluAlaAlaAlaAsnAlaGlnLys 88
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CCTGCCAGAAACATGCTGAAGATGGAATGGAACAAAGAGGCTGCAGCAAATGCCCAAAAG 240

Qy      89 TrpAlaAsnGlnCysAsnTyrArgHisSerAsnProLysAspArgMetThrSerLeuLys 108
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 TGGGCAAACCAGTGCAATTACAGACACAGTAACCCAAAGGATCGAATGACAAGTCTAAAA 300

Qy     109 CysGlyGluAsnLeuTyrMetSerSerAlaProSerSerTrpSerGlnAlaIleGlnSer 128
```

```
          ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db     301 TGTGGTGAGAATCTCTACATGTCAAGTGCCTCCAGCTCATGGTCACAAGCAATCCAAAGC 360

Qy     129 TrpPheAspGluTyrAsnAspPheAspPheGlyValGlyProLysThrProAsnAlaVal 148
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 TGGTTTGATGAGTACAATGATTTTGACTTTGGTGTAGGGCCAAAGACTCCCAACGCAGTG 420

Qy     149 ValGlyHisTyrThrGlnValValTrpTyrSerSerTyrLeuValGlyCysGlyAsnAla 168
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GTTGGACATTATACACAGGTTGTTTGGTACTCTTCATACCTCGTTGGATGTGGAAATGCC 480

Qy     169 TyrCysProAsnGlnLysValLeuLysTyrTyrTyrValCysGlnTyrCysProAlaGly 188
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TACTGTCCCAATCAAAAAGTTCTAAAATACTACTATGTTTGCCAATATTGTCCTGCTGGT 540

Qy     189 AsnTrpAlaAsnArgLeuTyrValProTyrGluGlnGlyAlaProCysAlaSerCysPro 208
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AATTGGGCTAATAGACTATATGTCCCTTATGAACAAGGAGCACCTTGTGCCAGTTGCCCA 600

Qy     209 AspAsnCysAspAspGlyLeuCysThrAsnGlyCysLysTyrGluAspLeuTyrSerAsn 228
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GATAACTGTGACGATGGACTATGCACCAATGGTTGCAAGTACGAAGATCTCTATAGTAAC 660

Qy     229 CysLysSerLeuLysLeuThrLeuThrCysLysHisGlnLeuValArgAspSerCysLys 248
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TGTAAAAGTTTGAAGCTCACATTAACCTGTAAACATCAGTTGGTCAGGGACAGTTGCAAG 720

Qy     249 AlaSerCysAsnCysSerAsnSerIleTyr 258
           |||||||||||||||||||||||||||||
Db     721 GCCTCCTGCAATTGTTCAAACAGCATTTAT 750
```

RESULT 12
AAS70843
ID AAS70843 standard; cDNA; 1386 BP.
XX
AC AAS70843;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #6647.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG06656.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 6647; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1386 BP; 438 A; 293 C; 289 G; 366 T; 0 other;

Alignment Scores:

Pred. No.:	1.94e-92	Length:	1386
Score:	1002.00	Matches:	184
Percent Similarity:	80.84%	Conservative:	27
Best Local Similarity:	70.50%	Mismatches:	45
Query Match:	69.78%	Indels:	5
DB:	23	Gaps:	3

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```
Qy       1 MetLysGlnIleLeuHisProAlaLeuGluThr-Thr------AlaMetThrLeuPhePr 18
           :::|||   |||   |||||||||   :::||| |||     ||||||   |||   ||
Db     195 ATAAAGTAGATATTTCATCCTGCTCAGAAAACCAACATTTCCAGCAATGGCTTTACTACC 254

Qy      18 oValLeuLeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAs 38
           ||||   ||||||||||||      ||||||||||||   ||||||   |||   |||||
Db     255 GGTG---TTGTTTCTGGTTACTGTGCTGCTTCCATCTTTACCTGCA---GAAGGAAAGGA 308

Qy      38 pProAlaPheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLy 58
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     309 TCCCGCTTTTACTGCTTTGTTAACCACCCAGTTGCAAGTGCAAAGGGAGATTGTAAATAA 368

Qy      58 sHisAsnGluLeuArgArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTr 78
           ||||||||||||||||:::||||||||||||||||||   ||||||||||||||||||||
Db     369 ACACAATGAACTAAGGAAAGCAGTCTCTCCACCTGCCAGTAACATGCTAAAGATGGAATG 428

Qy      78 pAsnLysGluAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSe 98
           |:::::|||         ||||||||||:::||||||||||:::|||      :::||||||
Db     429 GAGCAGAGAGGTAACAACGAATGCCCAAAGGTGGGCAAACAAGTGCACTTTACAACATAG 488

Qy      98 rAsnProLysAspArgMetThrSerLeuLysCysGlyGluAsnLeuTyrMetSerSerAl 118
           |:::|||:::||||||   ||||||   :::||||||||||||||||||||||||||||||
Db     489 TGATCCAGAGGACCGCAAAACCAGTACAAGATGTGGTGAGAATCTCTATATGTCAAGTGA 548

Qy     118 aProSerSerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAspPheAspPh 138
           |||:::||||||||||   ||||||||||||||:::||||||      ||||||   ::
Db     549 CCCTACTTCCTGGTCTTCTGCAATCCAAAGCTGGTATGACGAGATCCTAGATTTTGTCTA 608

Qy     138 eGlyValGlyProLysThrProAsnAlaValValGlyHisTyrThrGlnValValTrpTy 158
           :||||||||||||||:::||||||||||||||||||||||||||||||:::||||||||
Db     609 TGGTGTAGGACCAAAGAGTCCCAATGCAGTTGTTGGACATTATACTCAGCTTGTTTGGTA 668

Qy     158 rSerSerTyrLeuValGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuLysTy 178
           ||||:::|||   ||||||||||||   ||||||||||||||||||      ||||||||
Db     669 CTCGACTTACCAGGTAGGCTGTGGAATTGCCTACTGTCCCAATCAAGATAGTCTAAAATA 728

Qy     178 rTyrTyrValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeuTyrValProTy 198
           ||||||||||||||||||||||||||||||||||      ||||||      |||||
Db     729 CTACTATGTTTGCCAATATTGTCCTGCTGGTAATAATATGAATAGAAAGAATACCCCGTA 788

Qy     198 rGluGlnGlyAlaProCysAlaSerCysProAspAsnCysAspAspGlyLeuCysThrAs 218
           |:::||||||   |||||||||   ||||||||||:::||||||   ||||||||||||||
Db     789 CCAACAAGGAACACCTTGTGCCGGTTGCCCTGATGACTGTGACAAAGGACTATGCACCAA 848
```

```
Qy    218 nGlyCysLysTyrGluAspLeuTyrSerAsnCysLysSerLeuLysLeuThrLeuThrCy 238
          |   |||:::|||:::||||||   |||||||||   |||||||||   |||      ||
Db    849 TAGTTGCCAGTATCAAGATCTCCTAAGTAACTGTGATTCCTTGAAGAATACAGCTGGCTG 908

Qy    238 sLysHisGlnLeuValArgAspSerCysLysAlaSerCysAsnCysSerAsnSerIleTy 258
          |:::|||:::|||:::::::::   |||||||||:::|||   |||   |||   |||||
Db    909 TGAACATGAGTTACTCAAGGAAAAGTGCAAGGCTACTTGCCTATGTGAGAACAAAATTTA 968

Qy    258 r 258
          |
Db    969 C 969
```

RESULT 13
AAS92411
ID AAS92411 standard; cDNA; 1386 BP.
XX
AC AAS92411;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #28215.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG28224.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 28215; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 1386 BP; 438 A; 293 C; 289 G; 366 T; 0 other;

Alignment Scores:

Pred. No.:	1.94e-92	Length:	1386
Score:	1002.00	Matches:	184
Percent Similarity:	80.84%	Conservative:	27
Best Local Similarity:	70.50%	Mismatches:	45
Query Match:	69.78%	Indels:	5
DB:	23	Gaps:	3

US-09-698-781-3 (1-258) x AAS92411 (1-1386)

```
Qy      1 MetLysGlnIleLeuHisProAlaLeuGluThr-Thr------AlaMetThrLeuPhePr 18
          :::|||   |||   |||||||||   :::||| |||      ||||||   |||   ||
Db    195 ATAAAGTAGATATTTCATCCTGCTCAGAAAACCAACATTTCCAGCAATGGCTTTACTACC 254

Qy     18 oValLeuLeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAs 38
          ||||   ||||||||||||      ||||||||||||   ||||||   |||   |||||
Db    255 GGTG---TTGTTTCTGGTTACTGTGCTGCTTCCATCTTTACCTGCA---GAAGGAAAGGA 308

Qy     38 pProAlaPheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLy 58
          ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db    309 TCCCGCTTTTACTGCTTTGTTAACCACCCAGTTGCAAGTGCAAAGGGAGATTGTAAATAA 368

Qy     58 sHisAsnGluLeuArgArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTr 78
          ||||||||||||||:::||||||||||||||||||   ||||||||||||||||||||
Db    369 ACACAATGAACTAAGGAAAGCAGTCTCTCCACCTGCCAGTAACATGCTAAAGATGGAATG 428

Qy     78 pAsnLysGluAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSe 98
          |:::::|||          ||||||||:::|||||||||:::|||      :::||||||
Db    429 GAGCAGAGAGGTAACAACGAATGCCCAAAGGTGGGCAAACAAGTGCACTTTACAACATAG 488

Qy     98 rAsnProLysAspArgMetThrSerLeuLysCysGlyGluAsnLeuTyrMetSerSerAl 118
          |:::|||:::||||||   ||||||   :::|||||||||||||||||||||||||||||
Db    489 TGATCCAGAGGACCGCAAAACCAGTACAAGATGTGGTGAGAATCTCTATATGTCAAGTGA 548

Qy    118 aProSerSerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAspPheAspPh 138
          |||:::||||||||   ||||||||||||||:::||||||      ||||||   ::
Db    549 CCCTACTTCCTGGTCTTCTGCAATCCAAAGCTGGTATGACGAGATCCTAGATTTTGTCTA 608

Qy    138 eGlyValGlyProLysThrProAsnAlaValValGlyHisTyrThrGlnValValTrpTy 158
          :||||||||||||||:::||||||||||||||||||||||||||||||:::||||||||
Db    609 TGGTGTAGGACCAAAGAGTCCCAATGCAGTTGTTGGACATTATACTCAGCTTGTTTGGTA 668

Qy    158 rSerSerTyrLeuValGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuLysTy 178
          ||||:::|||   ||||||||||||   ||||||||||||||||||      ||||||||
Db    669 CTCGACTTACCAGGTAGGCTGTGGAATTGCCTACTGTCCCAATCAAGATAGTCTAAAATA 728

Qy    178 rTyrTyrValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeuTyrValProTy 198
          ||||||||||||||||||||||||||||||||      ||||||         |||||
Db    729 CTACTATGTTTGCCAATATTGTCCTGCTGGTAATAATATGAATAGAAAGAATACCCCGTA 788

Qy    198 rGluGlnGlyAlaProCysAlaSerCysProAspAsnCysAspAspGlyLeuCysThrAs 218
          |:::||||||   |||||||||   |||||||||:::||||||   ||||||||||||||
Db    789 CCAACAAGGAACACCTTGTGCCGGTTGCCCTGATGACTGTGACAAAGGACTATGCACCAA 848

Qy    218 nGlyCysLysTyrGluAspLeuTyrSerAsnCysLysSerLeuLysLeuThrLeuThrCy 238
          |   |||:::|||:::||||||   |||||||||   |||||||||   |||      ||
Db    849 TAGTTGCCAGTATCAAGATCTCCTAAGTAACTGTGATTCCTTGAAGAATACAGCTGGCTG 908

Qy    238 sLysHisGlnLeuValArgAspSerCysLysAlaSerCysAsnCysSerAsnSerIleTy 258
          |:::|||:::|||:::::::::   |||||||||:::|||   |||   |||   |||||
Db    909 TGAACATGAGTTACTCAAGGAAAAGTGCAAGGCTACTTGCCTATGTGAGAACAAAATTTA 968

Qy    258 r 258
          |
Db    969 C 969
```

RESULT 14
ABV43214/c
ID ABV43214 standard; cDNA; 534 BP.
XX
AC ABV43214;

```
XX
DT   16-SEP-2002  (first entry)
XX
DE   Human prostate expression marker cDNA 43205.
XX
KW   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW   pharmacogenomic marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200160860-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US05171.
XX
PR   17-FEB-2000; 2000US-183319P.
PR   16-MAR-2000; 2000US-189862P.
PR   25-MAY-2000; 2000US-207454P.
PR   09-JUN-2000; 2000US-211314P.
PR   18-JUL-2000; 2000US-219007P.
PR   13-DEC-2000; 2000US-255281P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Endege WO,  Monahan JE;
XX
DR   WPI; 2001-662795/76.
XX
PT   Novel isolated nucleic acid molecule associated with cancerous state of
PT   prostate cells and correlating with presence of prostate cancer, useful
PT   for detecting presence of prostate cancer, stage of prostate cancer  -
XX
PS   Claim 1; Page 8623; 11750pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (I) comprising
CC   a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC   specification or its complement. (I) is useful for:
CC   (a) assessing whether a patient is afflicted with prostate cancer;
CC   (b) monitoring the progression of prostate cancer in a patient;
CC   (c) assessing the efficacy of a test compound to inhibit prostate
CC   cancer in a patient;
CC   (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC   in a patient;
CC   (e) selecting a composition for inhibiting prostate cancer in a patient;
CC   (f) assessing the prostate cell carcinogenic potential of a compound;
CC   (g) determining whether prostate cancer has metastasized in a patient;
CC   (h) assessing the aggressiveness or indolence of prostate cancer in a
CC   patient;
CC   (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
XX
SQ   Sequence 534 BP; 120 A; 127 C; 133 G; 153 T; 1 other;

Alignment Scores:
Pred. No.:              1.87e-60        Length:         534
Score:                  683.00          Matches:        132
Percent Similarity:     98.51%          Conservative:   0
Best Local Similarity:  98.51%          Mismatches:     1
Query Match:            47.56%          Indels:         1
DB:                     23              Gaps:           0

US-09-698-781-3 (1-258) x ABV43214 (1-534)

Qy       1 MetLysGlnIleLeuHisProAlaLeuGluThrThrAlaMetThrLeuProProValLeu 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     434 ATGAAACAAATACTTCATCCTGCTCTGGAAACCACTGCAATGACATTATTCCCAGTGCTG 375

Qy      21 LeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAla 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     374 TTGTTCCTGGTTGCTGGGCTGCTTCCATCTTTTCCAGCAAATGAAGATAAGGATCCCGCT 315

Qy      41 PheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsn 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     314 TTTACTGCTTTGTTAACCACCCAAACACAAGTGCAAAGGGAGATTGTGAATAAGCACAAT 255

Qy      61 GluLeuArgArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLys 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     254 GAACTGAGGAGAGCAGTATCTCCCCCTGCCAGAAACATGCTGAAGATGGAATGGAACAAA 195

Qy      81 GluAlaAlaAlaAsnAlaGlnLysTrpAlaAsn-GlnCysAsnTyrArgHisSerAsnPr 100
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db     194 GAGGCTGCAGCAAATGCCCAAAAGTGGGCAAACNCAGTGCAATTACAGACACAGTAACCC 135

Qy     100 oLysAspArgMetThrSerLeuLysCysGlyGluAsnLeuTyrMetSerSerAlaProSe 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||
Db     134 AAAGGATCGAATGACAAGTCTAAAATGTGGTGAGAATCTCTACATGTCAAGTGCCTCCAG 75

Qy     120 rSerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyr 133
           |||||||||||||||||||||||||||||||||||||||
Db      74 CTCATGGTCACAAGCAATCCAAAGCTGGTTTGATGAGTAC 35

RESULT 15
AAS70842
ID   AAS70842 standard; cDNA; 683 BP.
XX
AC   AAS70842;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #6646.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG06655.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 1; SEQ ID No 6646; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human
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CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 683 BP; 215 A; 165 C; 141 G; 162 T; 0 other;

Alignment Scores:
Pred. No.:              2.98e-45        Length:         683
Score:                  535.50          Matches:        119
Percent Similarity:     64.73%          Conservative:   15
Best Local Similarity:  57.49%          Mismatches:     31
Query Match:            37.29%          Indels:         44
DB:                     23              Gaps:           4

US-09-698-781-3 (1-258) x AAS70842 (1-683)

Qy      1 MetLysGlnIleLeuHisProAlaLeuGluThr-Thr------AlaMetThrLeuPhePr 18
          :::|||   |||   |||||||||   :::||| |||      ||||||   |||   ||
Db    177 ATAAAGTAGATATTTCATCCTGCTCAGAAAACCAACATTTCCAGCAATGGCTTTACTACC 236

Qy     18 oValLeuLeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAs 38
          ||||   ||||||||||||      ||||||||||||   ||||||   |||   |||||
Db    237 GGTG---TTGTTTCTGGTTACTGTGCTGCTTCCATCTTTACCTGCA---GAAGGAAAGGA 290

Qy     38 pProAlaPheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLy 58
          |||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db    291 TCCCGCTTTTACTGCTTTGTTAACCACCCAGTTGCAAGTACAAAGGGAGATTGTAAATAA 350

Qy     58 sHisAsnGluLeuArgArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTr 78
          ||||||||||||||||:::||||||||||||||||   ||||||||||||||||||||
Db    351 ACACAATGAACTAAGGAAAGCAGTCTCTCCACCTGCCAGTAACATGCTAAAGATGGAATG 410

Qy     78 pAsnLysGluAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSe 98
          |::::::|||         |||||||||:::||||||||:::      |||   |||||
Db    411 GAGCAGAGAGGTAACAACGAATGCCCAAAGGTGGGCAAACAAGTCACTTTACAA-CATAG 469

Qy     98 rAsnProLysAspArgMetThrSerLeuLysCysGlyGluAsnLeuTyrMetSerSerAl 118
          |:::|||:::||||||   ||||||   :::||||||||||||||||||||||||||||
Db    470 TGATCCAGAGGACCGCAAAACCAGTACAAGATGTGGTGAGAATCTCTATATGTCAAGTGA 529

Qy    118 aProSerSerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAspPheAspPh 138
           |||:::|||||||||   |||||||||||||||:::||||||      ||||||   ::
Db    530 CCCTACTTCCTGGTCTTCTGCAATCCAAAGCTGGTATGACGAGATCCTAGATTTTGTCTA 589

Qy    138 eGlyValGlyProLysThrProAsnAlaValValGlyHisTyrThrGlnValValTrpTy 158
          :||||||||||||||:::|||
Db    590 TGGTGTAGGACCAAAGAGTCCCAA---------------------------------- 613

Qy    158 rSerSerTyrLeuValGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuLysTy 178

Db    613 ------------------------------------------------------------ 613

Qy    178 rTyrTyrValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeuTyrValProTy 198
                       ||||||||||||||||||      ||||||         |||||
Db    614 ---------------TATTGTCCTGCTGGTAATAATATGAATAGAAAGAATACCCCGTA 657

Qy    198 rGluGlnGlyAlaProCys 204
          |:::||||||   ||||||
Db    658 CCAACAAGGAACACCTTGT 676


Search completed: March 14, 2003, 03:17:52
Job time : 393.449 secs
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